



IFWO

RAW SEQUENCE LISTING

DATE: 09/17/2004

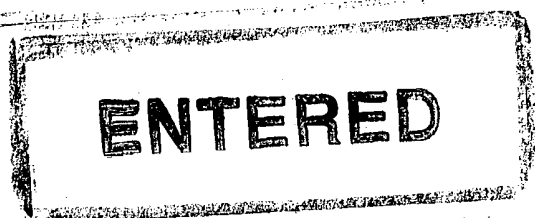
PATENT APPLICATION: US/10/770,600

TIME: 16:00:17

Input Set : A:\NuCycle-0021.ST25.txt

Output Set: N:\CRF4\09172004\J770600.raw

3 <110> APPLICANT: Fedorkin, et al.,
 5 <120> TITLE OF INVENTION: System for Expression of Genes in Plants
 7 <130> FILE REFERENCE: 2002645-0021
 9 <140> CURRENT APPLICATION NUMBER: 10/770,600
 10 <141> CURRENT FILING DATE: 2004-02-03
 12 <160> NUMBER OF SEQ ID NOS: 53
 14 <170> SOFTWARE: PatentIn version 3.2
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 28
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Primer SR22 was used to clone hGH without its leader, and
 23 introducing a PacI site at the 5' end.
 25 <400> SEQUENCE: 1
 26 ccggttaatta atgtcccaa ctattcca 28
 29 <210> SEQ ID NO: 2
 30 <211> LENGTH: 25
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Artificial
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: Primer SR23 was used to clone hGH with its leader.
 37 <400> SEQUENCE: 2
 38 ttaattaatg gcaactggat caagg 25
 41 <210> SEQ ID NO: 3
 42 <211> LENGTH: 24
 43 <212> TYPE: DNA
 44 <213> ORGANISM: Artificial
 46 <220> FEATURE:
 47 <223> OTHER INFORMATION: Primer SR24 was used to clone the hGH gene without KDEL and
 48 introducing a XhoI site at the 3' end.
 50 <400> SEQUENCE: 3
 51 cggctcgagt taaaaaccac atga 24
 54 <210> SEQ ID NO: 4
 55 <211> LENGTH: 30
 56 <212> TYPE: DNA
 57 <213> ORGANISM: Artificial
 59 <220> FEATURE:
 60 <223> OTHER INFORMATION: Primer SR25 was used to clone the gene with KDEL.
 62 <400> SEQUENCE: 4
 63 cggctcgagt tcattcttaa aacctgatcc 30
 66 <210> SEQ ID NO: 5
 67 <211> LENGTH: 42



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68 <212> TYPE: DNA
69 <213> ORGANISM: Artificial
71 <220> FEATURE:
72 <223> OTHER INFORMATION: XhoI site at 3' end of A peptide with KDEL.
74 <400> SEQUENCE: 5
75 cggctcgagt cagagttcat ctttggtaca gtagttctca ag          42
78 <210> SEQ ID NO: 6
79 <211> LENGTH: 36
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Primer used to modify GFP from Aequorea Victoria.
86 <400> SEQUENCE: 6
87 gggagatctt aattaatggc tagcaaagga gaagaa          36
90 <210> SEQ ID NO: 7
91 <211> LENGTH: 45
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Primer used to modify GFP from Aequorea Victoria.
98 <400> SEQUENCE: 7
99 cccctcgagc ggcgctgca gttatttgta gagctcatcc atgcc          45
102 <210> SEQ ID NO: 8
103 <211> LENGTH: 23
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Primer used to modify GFP from Aequorea Victoria.
110 <400> SEQUENCE: 8
111 gttccctggc caacacttgt cac          23
114 <210> SEQ ID NO: 9
115 <211> LENGTH: 22
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial
119 <220> FEATURE:
120 <223> OTHER INFORMATION: Primer used to modify GFP from Aequorea Victoria.
122 <400> SEQUENCE: 9
123 tagtgacaag tgttgccag gg          22
126 <210> SEQ ID NO: 10
127 <211> LENGTH: 25
128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Primer used to modify GFP from Aequorea Victoria.
134 <400> SEQUENCE: 10
135 ggacacaaac tggagtacaa ctata          25
138 <210> SEQ ID NO: 11
139 <211> LENGTH: 25
140 <212> TYPE: DNA

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141 <213> ORGANISM: Artificial
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Primer used to modify GFP from Aequorea Victoria.
146 <400> SEQUENCE: 11
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150 <210> SEQ ID NO: 12
151 <211> LENGTH: 33
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Primer related to Alfalfa Mosaic virus
158 <400> SEQUENCE: 12
159 ccgctcgagc tgcagtgtac cccattaatt tgg 33
162 <210> SEQ ID NO: 13
163 <211> LENGTH: 35
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Primer related to Alfalfa mosaic virus.
170 <400> SEQUENCE: 13
171 cgggtcgacg cggccgcaaa taggacttca tacct 35
174 <210> SEQ ID NO: 14
175 <211> LENGTH: 35
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Primer related to Alfalfa mosaic virus.
182 <400> SEQUENCE: 14
183 cgggtcgacg cggccgcaat atgaagtcga tccta 35
186 <210> SEQ ID NO: 15
187 <211> LENGTH: 35
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial
191 <220> FEATURE:
192 <223> OTHER INFORMATION: Primer related to Alfalfa mosaic virus.
194 <400> SEQUENCE: 15
195 cgggtcgacg cggccgca tcccttaggg gcatt 35
198 <210> SEQ ID NO: 16
199 <211> LENGTH: 424
200 <212> TYPE: PRT
201 <213> ORGANISM: Tobamovirus/TMV-KR
203 <400> SEQUENCE: 16
205 Lys Gln Met Ser Ile Val Tyr Thr Gly Pro Ile Lys Val Gln Gln
206 1 5 10 15
209 Met Lys Asn Phe Ile Asp Ser Leu Val Ala Ser Leu Ser Ala Val
210 20 25 30
213 Ser Asn Leu Val Lys Ile Leu Lys Asp Thr Ala Ala Ile Asp Leu Glu
214 35 40 45
217 Thr Arg Gln Lys Phe Gly Val Leu Asp Val Ala Ser Arg Lys Trp Leu

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218      50      55      60
221 Ile Lys Pro Thr Ala Lys Ser His Ala Trp Gly Val Val Glu Thr His
222 65      70      75      80
225 Ala Arg Lys Tyr His Val Ala Leu Leu Glu Tyr Asp Glu Gln Gly Val
226      85      90      95
229 Val Thr Cys Asp Asn Trp Arg Arg Val Ala Val Ser Ser Glu Ser Val
230      100      105      110
233 Val Tyr Ser Asp Met Ala Lys Leu Arg Thr Leu Arg Arg Leu Leu Arg
234      115      120      125
237 Asn Gly Glu Pro His Val Ser Ser Ala Lys Val Val Leu Val Asp Gly
238      130      135      140
241 Val Pro Gly Cys Gly Lys Thr Lys Glu Ile Leu Ser Arg Val Asn Phe
242 145      150      155      160
245 Asp Glu Asp Leu Ile Leu Val Pro Gly Lys Gln Ala Ala Glu Met Ile
246      165      170      175
249 Arg Arg Arg Ala Asn Ser Ser Gly Ile Ile Val Ala Thr Lys Asp Asn
250      180      185      190
253 Val Lys Thr Val Asp Ser Phe Met Met Asn Phe Gly Lys Ser Thr Arg
254      195      200      205
257 Cys Gln Phe Lys Arg Leu Phe Ile Asp Glu Gly Leu Met Leu His Thr
258      210      215      220
261 Gly Cys Val Asn Phe Leu Val Thr Met Ser Leu Cys Glu Ile Ala Tyr
262 225      230      235      240
265 Val Tyr Gly Asp Thr Gln Gln Ile Pro Tyr Ile Asn Arg Val Ser Gly
266      245      250      255
269 Phe Pro Tyr Pro Ala His Phe Ala Lys Leu Glu Val Asp Glu Val Glu
270      260      265      270
273 Thr Arg Arg Thr Thr Leu Arg Cys Pro Ala Asp Val Thr His Tyr Leu
274      275      280      285
277 Asn Arg Arg Tyr Glu Gly Phe Val Met Ser Thr Ser Ser Val Lys Lys
278      290      295      300
281 Ser Val Ser Gln Glu Met Val Gly Gly Ala Ala Val Ile Asn Pro Ile
282 305      310      315      320
285 Ser Lys Pro Leu His Gly Lys Ile Leu Thr Phe Thr Gln Ser Asp Lys
286      325      330      335
289 Glu Ala Leu Leu Ser Arg Gly Tyr Ser Asp Val His Thr Val His Glu
290      340      345      350
293 Val Gln Gly Glu Thr Tyr Ser Asp Val Ser Leu Val Arg Leu Thr Pro
294      355      360      365
297 Thr Pro Val Ser Ile Ile Ala Gly Asp Ser Pro His Val Leu Val Ala
298      370      375      380
301 Leu Ser Arg His Thr Cys Ser Leu Lys Tyr Tyr Thr Val Val Met Asp
302 385      390      395      400
305 Pro Leu Val Ser Ile Arg Asp Leu Glu Lys Leu Ser Ser Tyr Leu
306      405      410      415
309 Leu Asp Met Tyr Lys Val Asp Ala
310      420
313 <210> SEQ ID NO: 17
314 <211> LENGTH: 424

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315 <212> TYPE: PRT
316 <213> ORGANISM: Tobamovirus/TMV-RAK
318 <400> SEQUENCE: 17
320 Lys Gln Met Ser Ser Ile Val Tyr Thr Gly Pro Ile Lys Val Gln Gln
321 1 5 10 15
324 Met Lys Asn Phe Ile Asp Ser Leu Val Ala Ser Leu Ser Ala Ala Val
325 20 25 30
328 Ser Asn Leu Val Lys Ile Leu Lys Asp Thr Ala Ala Ile Asp Leu Glu
329 35 40 45
332 Thr Arg Gln Lys Phe Gly Val Leu Asp Val Ala Ser Arg Lys Trp Leu
333 50 55 60
336 Ile Lys Pro Thr Ala Lys Ser His Ala Trp Gly Val Val Glu Thr His
337 65 70 75 80
340 Ala Arg Lys Tyr His Val Ala Leu Leu Glu Tyr Asp Glu Gln Gly Ile
341 85 90 95
344 Val Thr Cys Asp Asp Trp Arg Arg Val Ala Val Ser Ser Glu Ser Val
345 100 105 110
348 Val Tyr Ser Asp Met Ala Lys Leu Arg Thr Leu Arg Arg Leu Leu Arg
349 115 120 125
352 Asp Gly Glu Pro His Val Ser Asn Ala Lys Val Val Leu Val Asp Gly
353 130 135 140
356 Val Pro Gly Cys Gly Lys Thr Lys Glu Ile Leu Ser Arg Val Asn Phe
357 145 150 155 160
360 Asp Glu Asp Leu Ile Leu Val Pro Gly Lys Gln Ala Ala Glu Met Ile
361 165 170 175
364 Arg Arg Arg Ala Asn Ser Ser Gly Ile Ile Val Ala Thr Lys Asp Asn
365 180 185 190
368 Val Arg Thr Val Asp Ser Phe Met Met Asn Phe Gly Lys Thr Thr Arg
369 195 200 205
372 Cys Gln Phe Lys Arg Leu Phe Ile Asp Glu Gly Leu Met Leu His Thr
373 210 215 220
376 Gly Cys Val Asn Phe Leu Val Ala Met Ser Leu Cys Asp Val Ala Tyr
377 225 230 235 240
380 Val Tyr Gly Asp Thr Gln Gln Ile Pro Tyr Ile Asn Arg Val Ser Gly
381 245 250 255
384 Phe Pro Tyr Pro Ala His Phe Ser Lys Leu Glu Val Asp Glu Val Glu
385 260 265 270
388 Thr Arg Arg Thr Thr Leu Arg Cys Pro Ala Asp Val Thr His Tyr Leu
389 275 280 285
392 Asn Arg Arg Tyr Glu Gly Phe Val Val Ser Thr Ser Ser Val Lys Lys
393 290 295 300
396 Ser Val Ser Gln Glu Met Val Ser Gly Ala Ala Val Ile Asn Pro Ile
397 305 310 315 320
400 Ser Lys Pro Leu His Gly Lys Ile Leu Thr Phe Thr Gln Ser Asp Lys
401 325 330 335
404 Glu Ala Leu Leu Ser Arg Gly Tyr Ser Glu Val His Thr Val His Glu
405 340 345 350
408 Val Gln Gly Glu Thr Tyr Ser Asp Val Ser Leu Val Arg Leu Thr Pro
409 355 360 365

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RAW SEQUENCE LISTING ERROR SUMMARY

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15

VERIFICATION SUMMARY

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